

# Design of a duplex-probe n-mer array

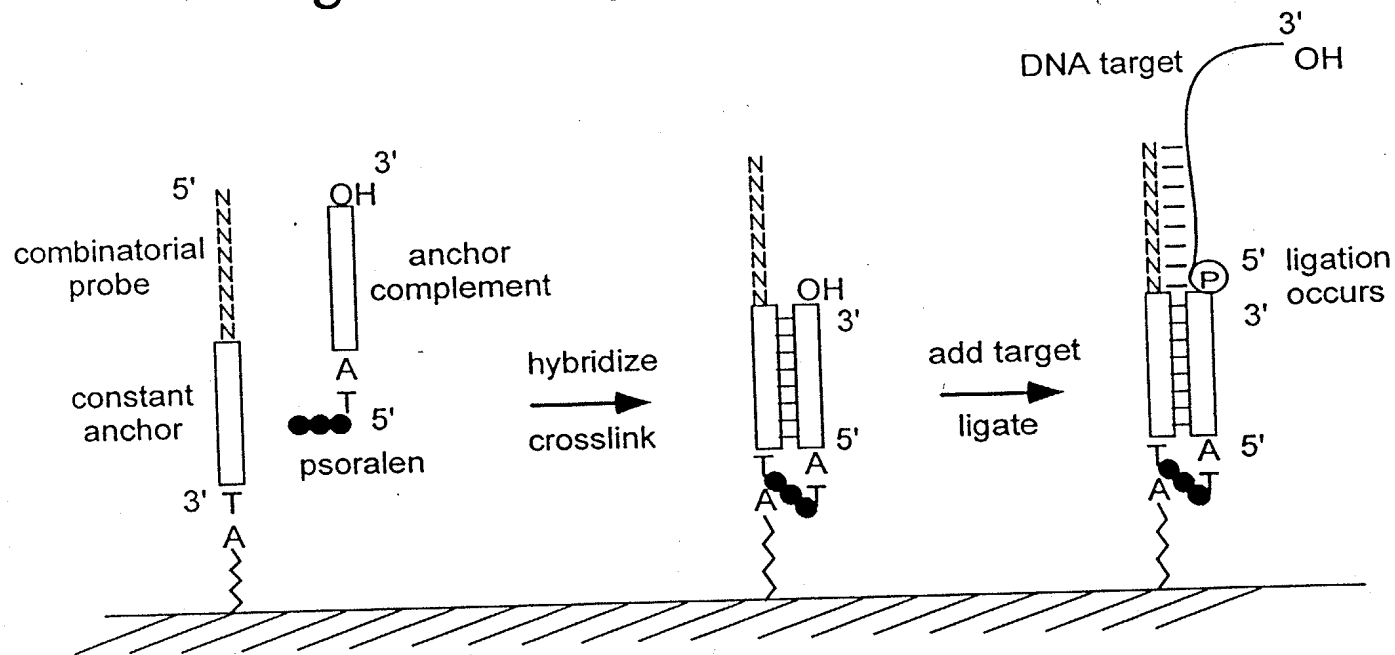


Fig. 1

Ligation of a 1.2 kb HIV amplicon to an 8-mer array.

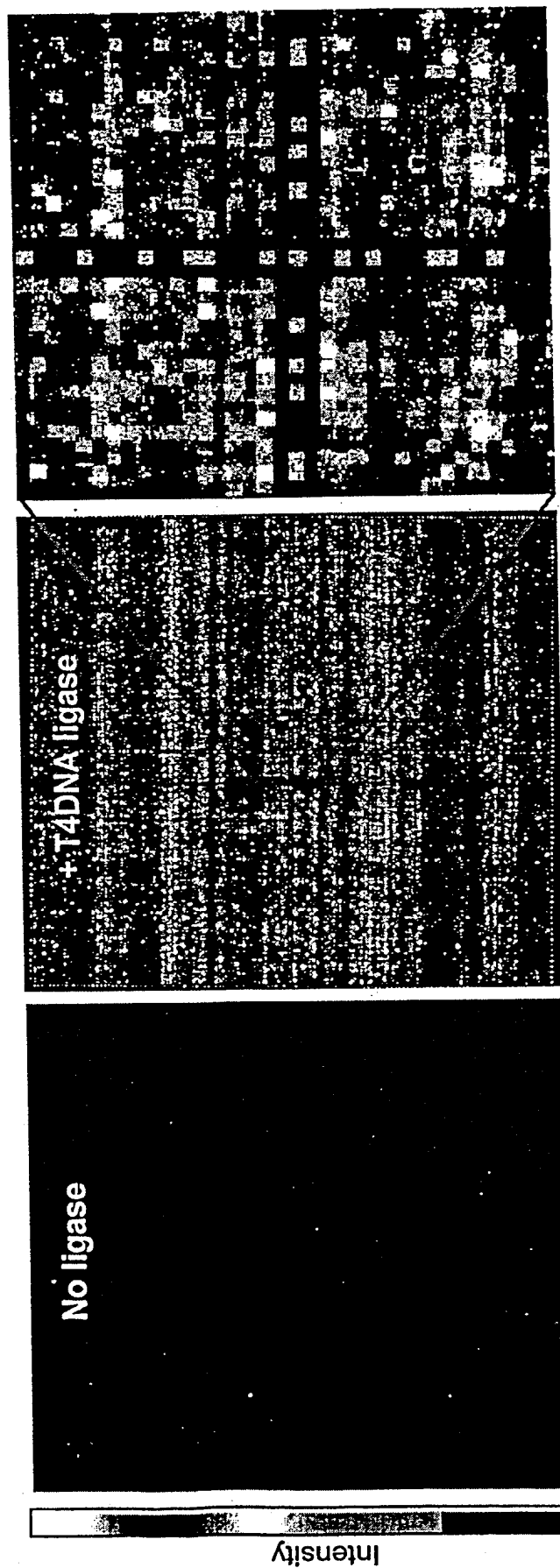


Fig. 2a

Fig. 2b

Fig. 2c

# Construction of base call sets using a reference sequence

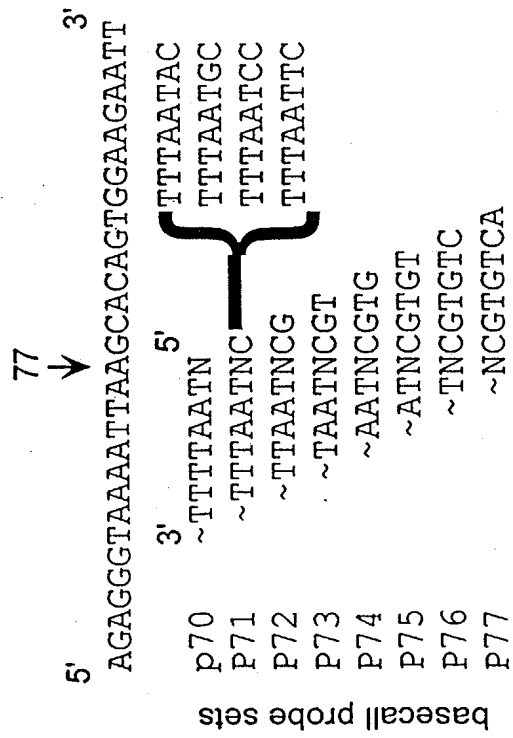


Fig. 3a

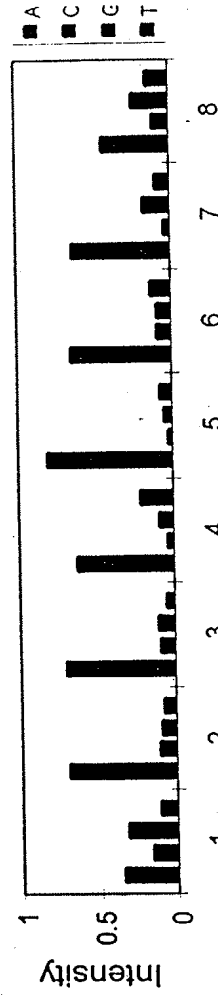


Fig. 3b

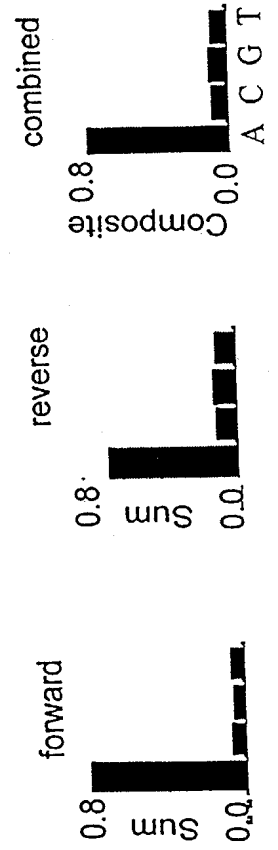


Fig. 3c

# Display of base call information in a "sequencing trace"

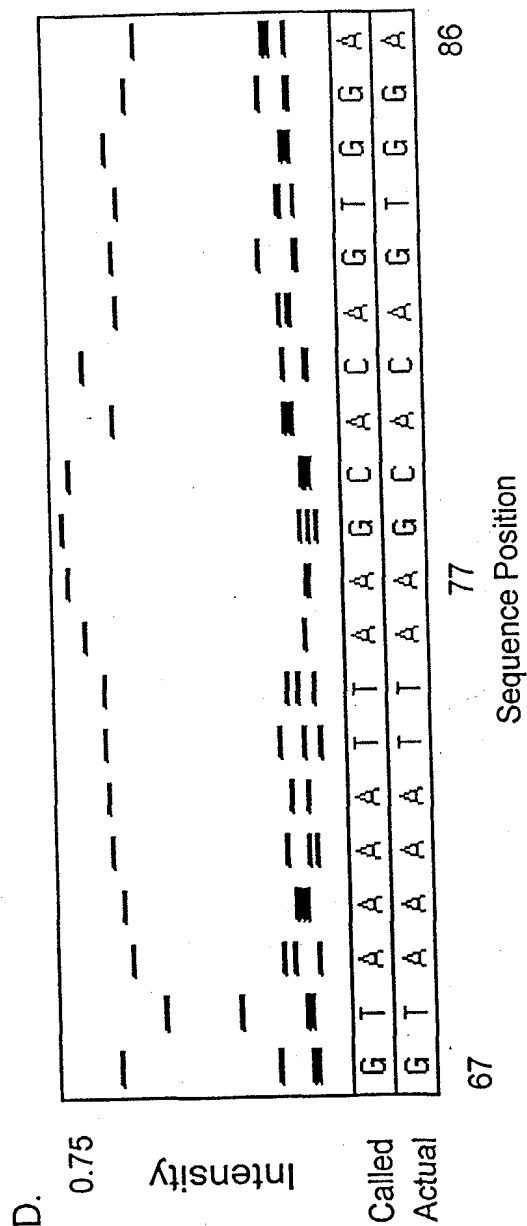


Fig. 4

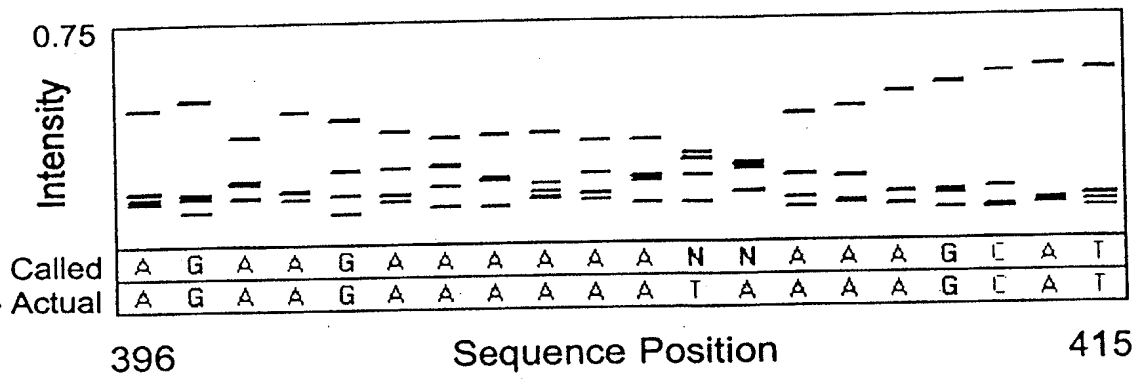


Fig. 5a

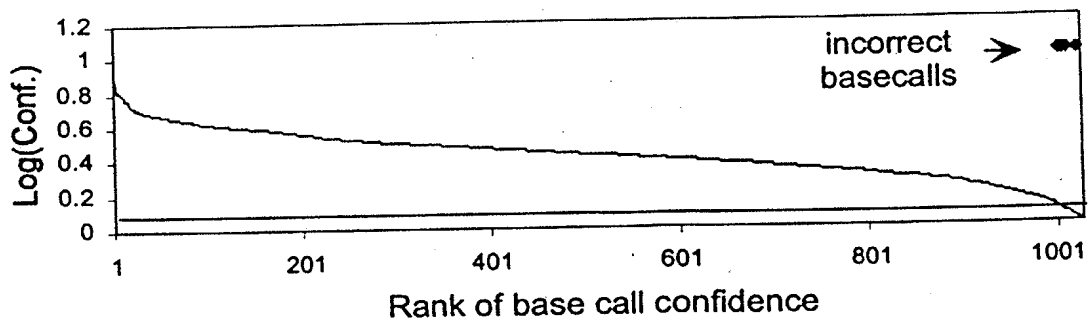


Fig. 5b

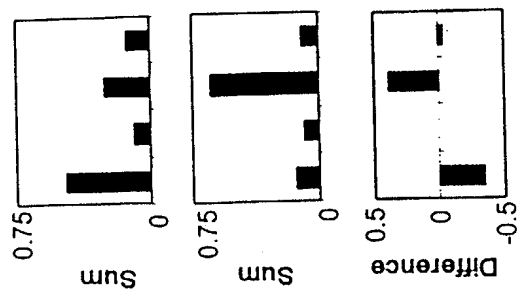
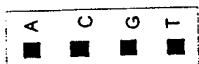
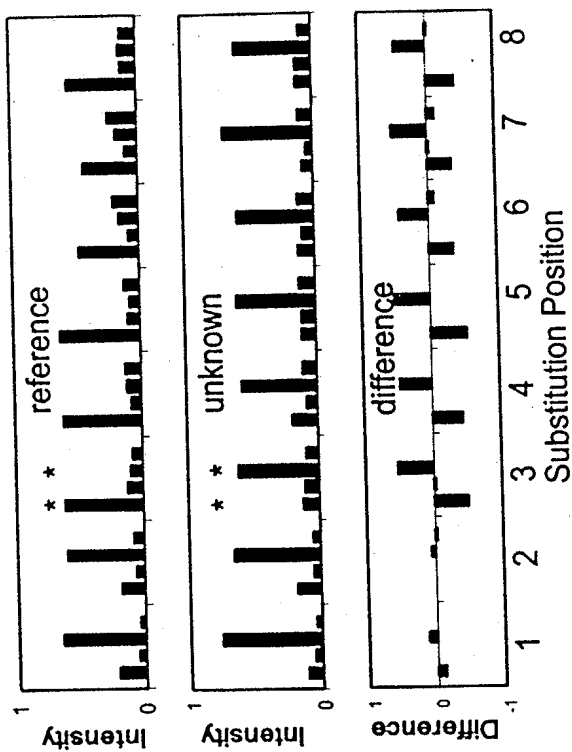
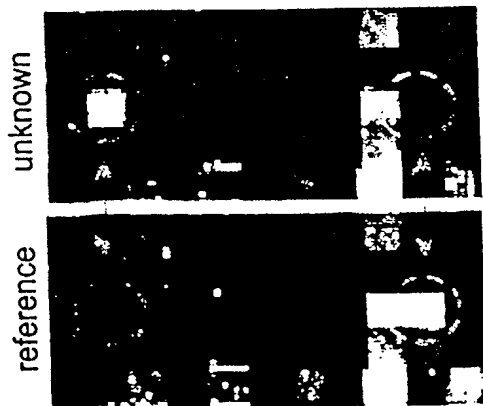


Fig. 6a

Fig. 6b

Fig. 6c

Direct comparison of sequence traces allows easy identification of a mutation.

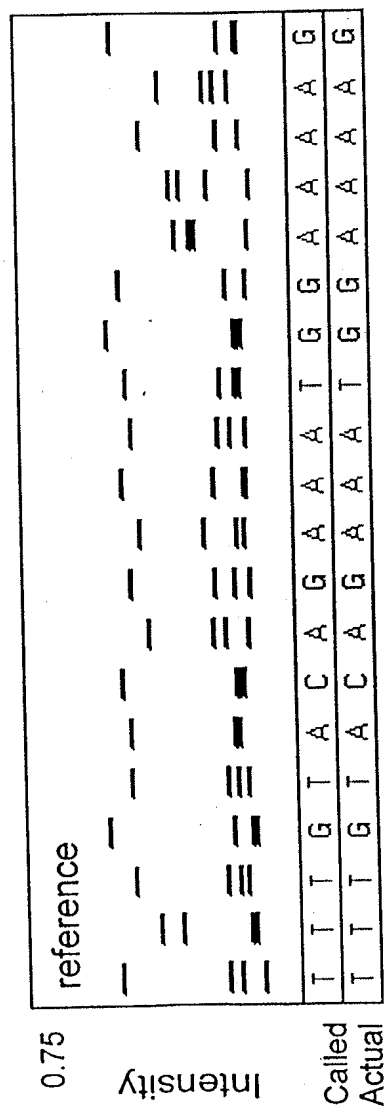


Fig. 7a

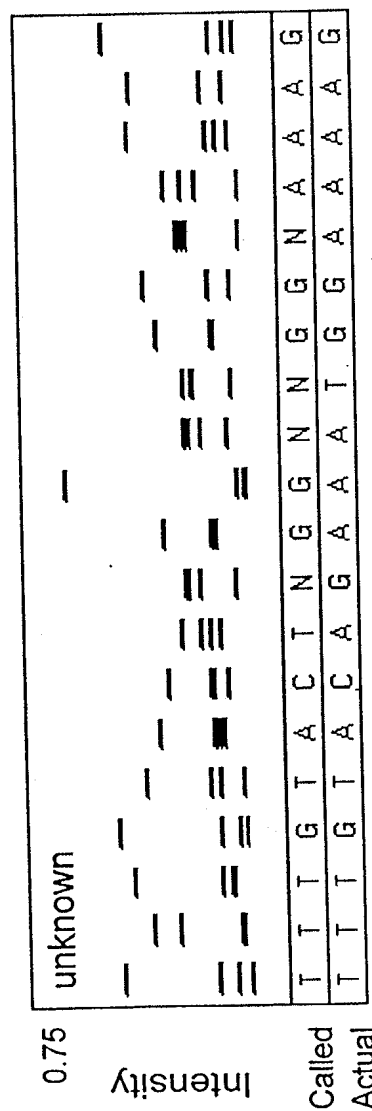


Fig. 7b

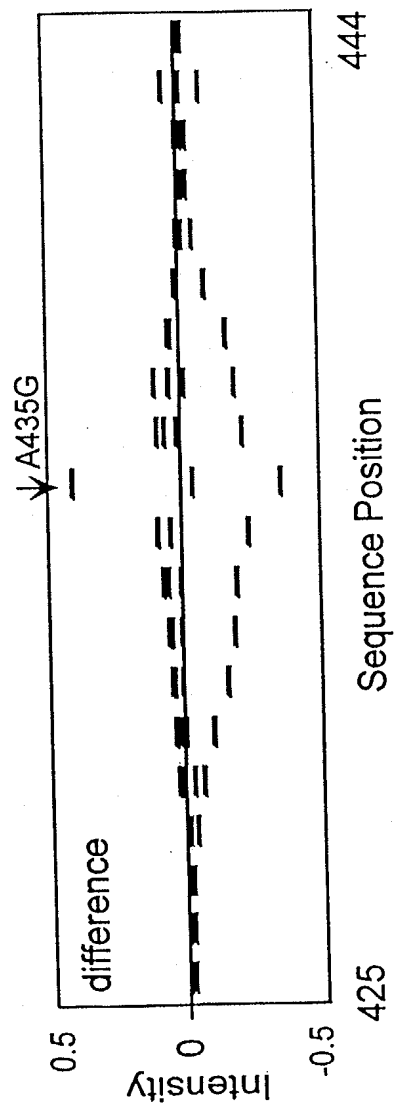


Fig. 7c

# Mutation scan of 1041 bases in HIV pol-1 gene

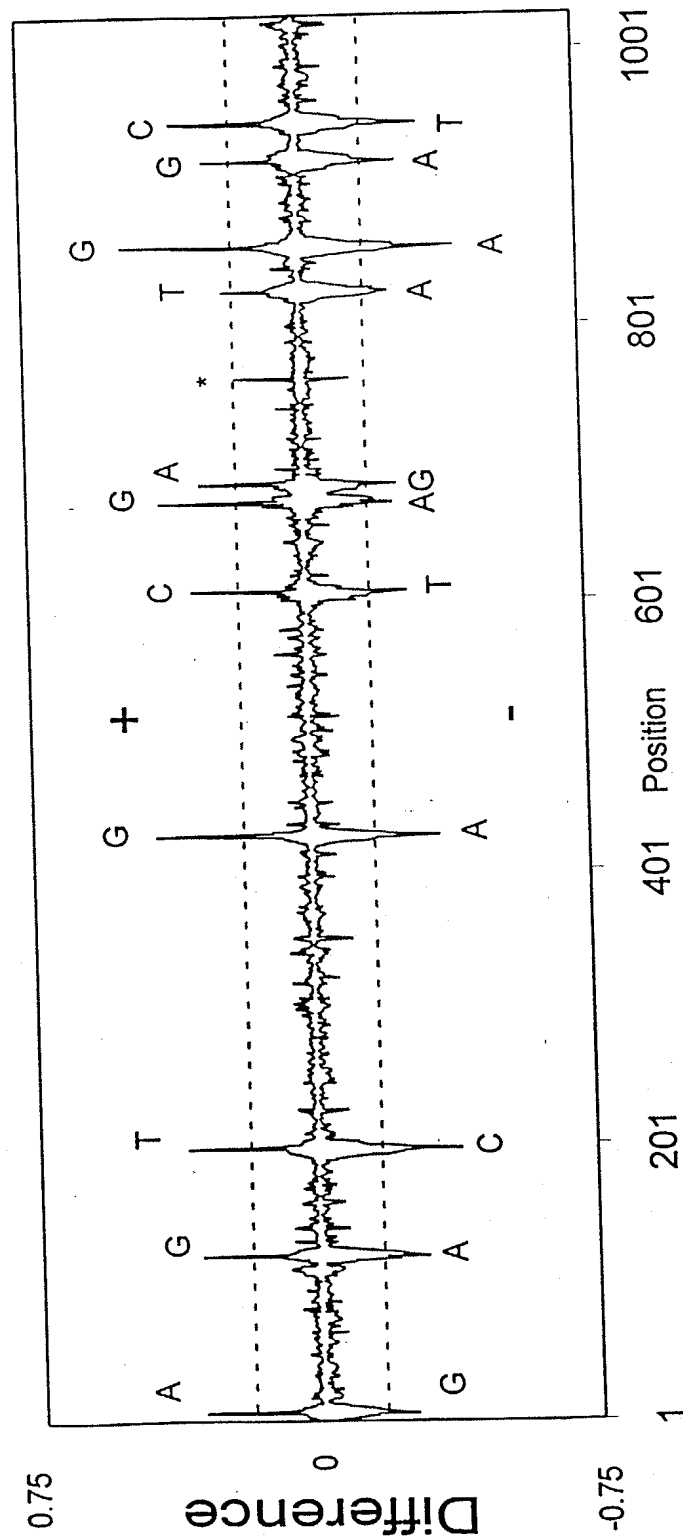


Fig. 8



# Detection of an insertion in the p53 gene

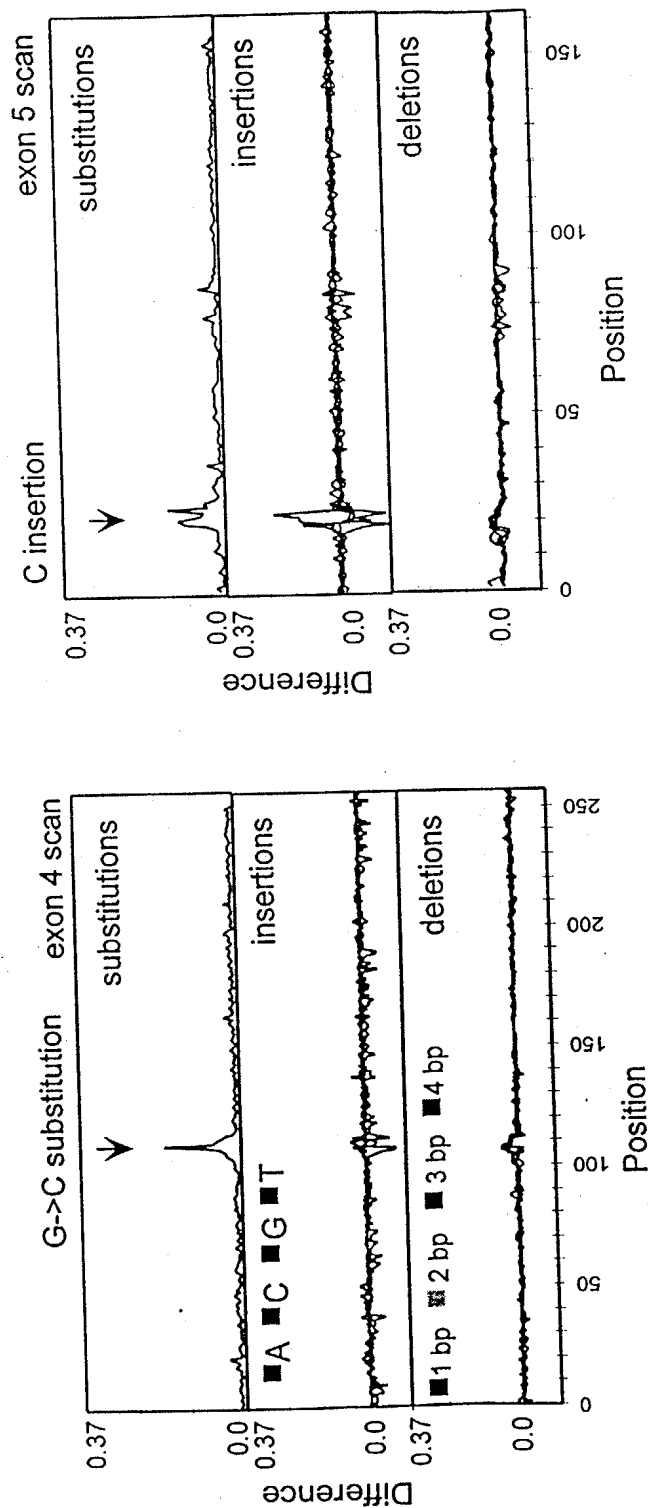


Fig. 9a

Fig. 9b

# Detection of the $\Delta$ F508 heterozygous deletion in the CFTR gene

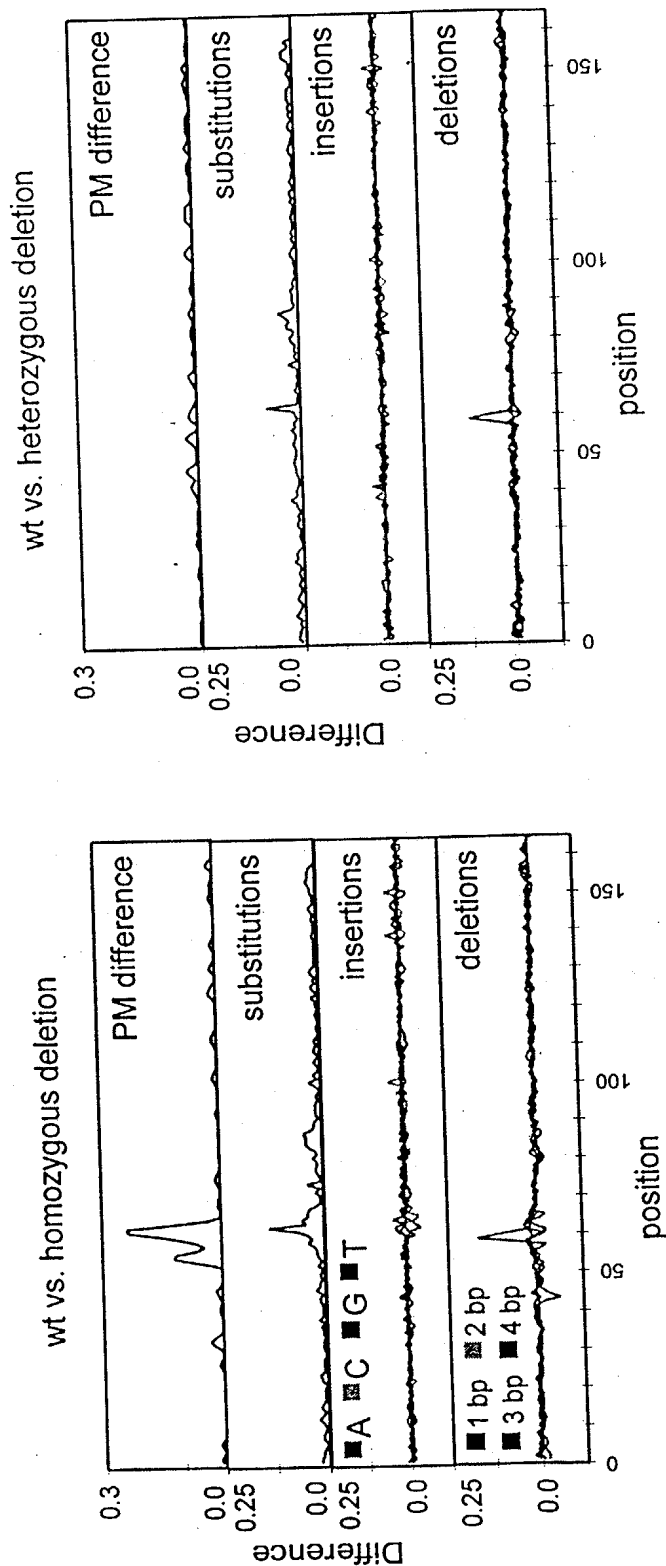


Fig. 10a

Fig. 10b

# Mutation scan of 2.5 kbp mitochondrial amplicons (homozygous vs. heterozygous)

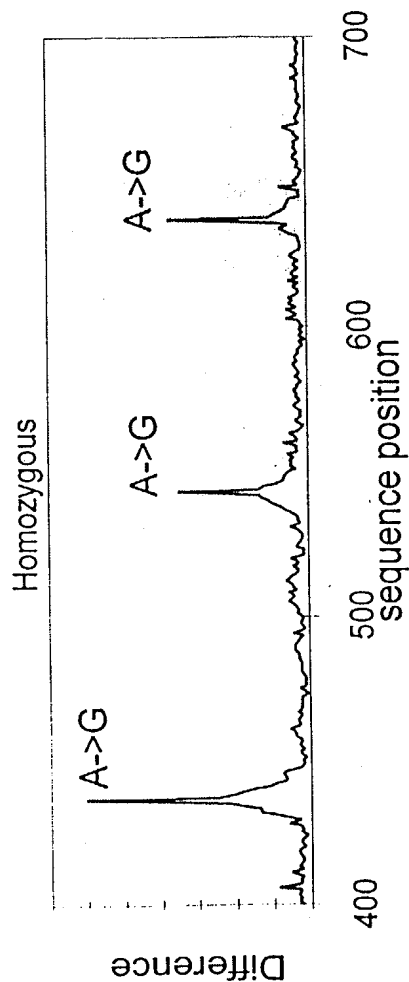


Fig. 11a

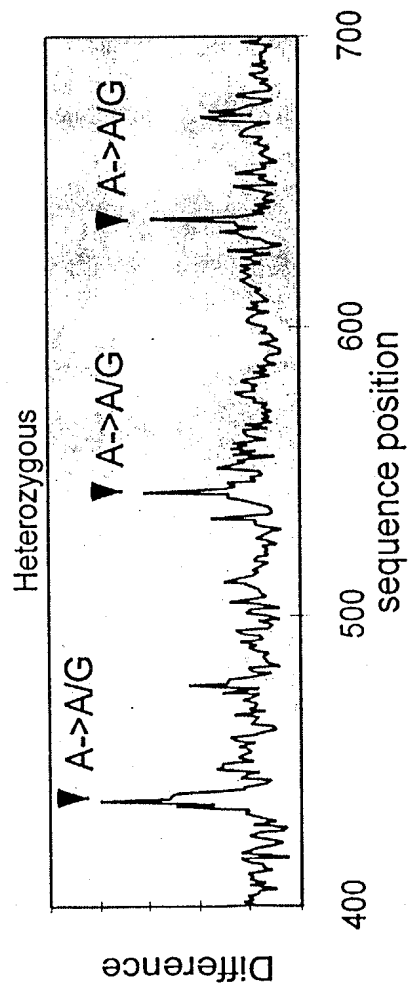


Fig. 11b